



IFW16

RAW SEQUENCE LISTING

DATE: 10/04/2004

PATENT APPLICATION: US/10/632,694A

TIME: 11:02:44

Input Set : A:\New SURR113.ST25.txt

Output Set: N:\CRF4\10042004\J632694A.raw

3 <110> APPLICANT: Allison, Anthony
 5 <120> TITLE OF INVENTION: MODIFIED ANNEXIN PROTEINS AND METHODS FOR TREATING VASO-
 OCCLUSIVE

6 SICKLE-CELL DISEASE

8 <130> FILE REFERENCE: SURR.113

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/632,694A

C--> 10 <141> CURRENT FILING DATE: 2003-08-01

10 <150> PRIOR APPLICATION NUMBER: 60/400,718

11 <151> PRIOR FILING DATE: 2002-08-02

13 <150> PRIOR APPLICATION NUMBER: 10/080,370

14 <151> PRIOR FILING DATE: 2002-02-21

16 <160> NUMBER OF SEQ ID NOS: 9

18 <170> SOFTWARE: PatentIn version 3.2

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 957

22 <212> TYPE: DNA

23 <213> ORGANISM: Homo sapiens

25 <400> SEQUENCE: 1

26 gcacaggttc tcagagggcac tgtgactgac ttccctggat ttgatgagcg ggctgatgca 60
 28 gaaactcttc ggaaggctat gaaaggcttg ggcacagatg aggagagcat cctgactctg 120
 30 ttgacatccc gaagtaatgc tcagcgccag gaaatctctg cagcttttaa gactctgttt 180
 32 ggcagggatc ttctggatga cctgaaatca gaactaactg gaaaatttga aaaattaatt 240
 34 gtggctctga tgaaaccctc tcggctttat gatgcttatg aactgaaaca tgccttgaag 300
 36 ggagctggaa caaatgaaaa agtactgaca gaaattattg cttcaaggac acctgaagaa 360
 38 ctgagagcca tcaaacaagt ttatgaagaa gaatatggct caagcctgga agatgacgtg 420
 40 gtgggggaca cttcagggtg ctaccagcgg atgttggtgg ttctccttca ggctaacaga 480
 42 gaccctgatg ctggaattga tgaagctcaa gttgaacaag atgctcaggc tttatttcag 540
 44 gctggagaac ttaaatgggg gacagatgaa gaaaagttaa tcaccatctt tggaacacga 600
 46 agtgtgtctc atttgagaaa ggtgtttgac aagtacatga ctatatcagg atttcaaatt 660
 48 gaggaacca ttgaccgcga gacttctggc aatttagagc aactactcct tgctgttggtg 720
 50 aaatctattc gaagtatacc tgcctacctt gcagagaccc tctattatgc tatgaaggga 780
 52 gctgggacag atgatcatat cctcatcaga gtcatgggtt ccaggagtga gattgatctg 840
 54 tttaacatca ggaaggagtt taggaagaat tttgccacct ctctttattc catgattaag 900
 56 ggagatacat ctgggggacta taagaaagct cttctgctgc tctgtggaga agatgac 957

59 <210> SEQ ID NO: 2

60 <211> LENGTH: 957

61 <212> TYPE: DNA

62 <213> ORGANISM: Homo sapiens

65 <220> FEATURE:

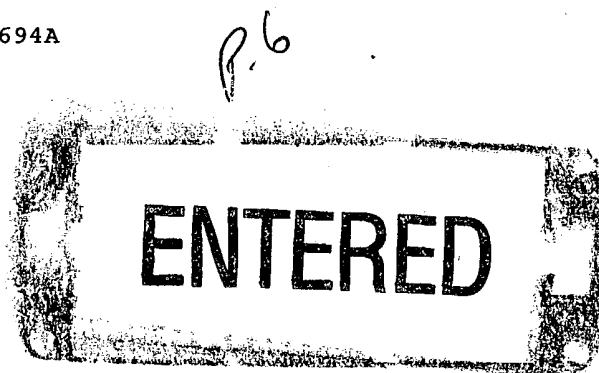
66 <221> NAME/KEY: CDS

67 <222> LOCATION: (1)..(957)

69 <400> SEQUENCE: 2

70 gca cag gtt ctg aga ggc act gtg act gac ttc cct gga ttt gat gag 48

71 Ala Gln Val Leu Arg Gly Thr Val Thr Asp Phe Pro Gly Phe Asp Glu



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72 1          5          10          15
74 cgg gct gat gca gaa act ctt cgg aag gct atg aaa ggc ttg ggc aca 96
75 Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys Gly Leu Gly Thr
76          20          25          30
78 gat gag gag agc atc ctg act ctg ttg aca tcc cga agt aat gct cag 144
79 Asp Glu Glu Ser Ile Leu Thr Leu Leu Thr Ser Arg Ser Asn Ala Gln
80          35          40          45
82 cgc cag gaa atc tct gca gct ttt aag act ctg ttt ggc agg gat ctt 192
83 Arg Gln Glu Ile Ser Ala Ala Phe Lys Thr Leu Phe Gly Arg Asp Leu
84          50          55          60
86 ctg gat gac ctg aaa tca gaa cta act gga aaa ttt gaa aaa tta att 240
87 Leu Asp Asp Leu Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile
88 65          70          75          80
90 gtg gct ctg atg aaa ccc tct cgg ctt tat gat gct tat gaa ctg aaa 288
91 Val Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys
92          85          90          95
94 cat gcc ttg aag gga gct gga aca aat gaa aaa gta ctg aca gaa att 336
95 His Ala Leu Lys Gly Ala Gly Thr Asn Glu Lys Val Leu Thr Glu Ile
96          100          105          110
98 att gct tca agg aca cct gaa gaa ctg aga gcc atc aaa caa gtt tat 384
99 Ile Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Val Tyr
100          115          120          125
102 gaa gaa gaa tat ggc tca agc ctg gaa gat gac gtg gtg ggg gac act 432
103 Glu Glu Glu Tyr Gly Ser Ser Leu Glu Asp Asp Val Val Gly Asp Thr
104          130          135          140
106 tca ggg tac tac cag cgg atg ttg gtg gtt ctc ctt cag gct aac aga 480
107 Ser Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg
108 145          150          155          160
110 gac cct gat gct gga att gat gaa gct caa gtt gaa caa gat gct cag 528
111 Asp Pro Asp Ala Gly Ile Asp Glu Ala Gln Val Glu Gln Asp Ala Gln
112          165          170          175
114 gct tta ttt cag gct gga gaa ctt aaa tgg ggg aca gat gaa gaa aag 576
115 Ala Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys
116          180          185          190
118 ttt atc acc atc ttt gga aca cga agt gtg tct cat ttg aga aag gtg 624
119 Phe Ile Thr Ile Phe Gly Thr Arg Ser Val Ser His Leu Arg Lys Val
120          195          200          205
122 ttt gac aag tac atg act ata tca gga ttt caa att gag gaa acc att 672
123 Phe Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile
124          210          215          220
126 gac cgc gag act tct ggc aat tta gag caa cta ctc ctt gct gtt gtg 720
127 Asp Arg Glu Thr Ser Gly Asn Leu Glu Gln Leu Leu Leu Ala Val Val
128 225          230          235          240
130 aaa tct att cga agt ata cct gcc tac ctt gca gag acc ctc tat tat 768
131 Lys Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr
132          245          250          255
134 gct atg aag gga gct ggg aca gat gat cat acc ctc atc aga gtc atg 816
135 Ala Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Met
136          260          265          270

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138 gtt tcc agg agt gag att gat ctg ttt aac atc agg aag gag ttt agg      864
139 Val Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg
140      275      280      285
142 aag aat ttt gcc acc tct ctt tat tcc atg att aag gga gat aca tct      912
143 Lys Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser
144      290      295      300
146 ggg gac tat aag aaa gct ctt ctg ctg ctc tgt gga gaa gat gac      957
147 Gly Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Glu Asp Asp
148 305      310      315
151 <210> SEQ ID NO: 3
152 <211> LENGTH: 319
153 <212> TYPE: PRT
154 <213> ORGANISM: Homo sapiens
156 <400> SEQUENCE: 3
158 Ala Gln Val Leu Arg Gly Thr Val Thr Asp Phe Pro Gly Phe Asp Glu
159 1      5      10      15
162 Arg Ala Asp Ala Glu Thr Leu Arg Lys Ala Met Lys Gly Leu Gly Thr
163      20      25      30
166 Asp Glu Glu Ser Ile Leu Thr Leu Thr Ser Arg Ser Asn Ala Gln
167      35      40      45
170 Arg Gln Glu Ile Ser Ala Ala Phe Lys Thr Leu Phe Gly Arg Asp Leu
171      50      55      60
174 Leu Asp Asp Leu Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile
175 65      70      75      80
178 Val Ala Leu Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys
179      85      90      95
182 His Ala Leu Lys Gly Ala Gly Thr Asn Glu Lys Val Leu Thr Glu Ile
183      100      105      110
186 Ile Ala Ser Arg Thr Pro Glu Glu Leu Arg Ala Ile Lys Gln Val Tyr
187      115      120      125
190 Glu Glu Glu Tyr Gly Ser Ser Leu Glu Asp Asp Val Val Gly Asp Thr
191      130      135      140
194 Ser Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg
195 145      150      155      160
198 Asp Pro Asp Ala Gly Ile Asp Glu Ala Gln Val Glu Gln Asp Ala Gln
199      165      170      175
202 Ala Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys
203      180      185      190
206 Phe Ile Thr Ile Phe Gly Thr Arg Ser Val Ser His Leu Arg Lys Val
207      195      200      205
210 Phe Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile
211      210      215      220
214 Asp Arg Glu Thr Ser Gly Asn Leu Glu Gln Leu Leu Leu Ala Val Val
215 225      230      235      240
218 Lys Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr
219      245      250      255
222 Ala Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Met
223      260      265      270
226 Val Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg

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227          275          280          285
230 Lys Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser
231          290          295          300
234 Gly Asp Tyr Lys Lys Ala Leu Leu Leu Cys Gly Glu Asp Asp
235 305          310          315
238 <210> SEQ ID NO: 4
239 <211> LENGTH: 2016
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: primer
247 <220> FEATURE:
248 <221> NAME/KEY: misc_feature
249 <222> LOCATION: (45)..(45)
250 <223> OTHER INFORMATION: n = a, c, t, or g
252 <220> FEATURE:
253 <221> NAME/KEY: misc_feature
254 <222> LOCATION: (1000)..(1002)
255 <223> OTHER INFORMATION: n = a, c, t, or g
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (1051)..(1053)
260 <223> OTHER INFORMATION: n = a, c, t, or g
262 <400> SEQUENCE: 4
--> 263 atggactaca aagacgatga cgacaagctt gggccgcga attngccct gcgcggcacc 60
265 gtgaccgact tctccggctt cgacggccgc gccgacgcc aggtgctgcg caaggccatg 120
267 aagggcctgg gcaccgacga ggactccatc ctgaacctgc tgaccgcccg ctccaacgcc 180
269 cagcgccagc agatcgccga ggagtccaag accctgttcg gccgcgacct ggtgaacgac 240
271 atgaagtccg agctgaccgg caagttcgag aagctgatcg tggccctgat gaagccctcc 300
273 cgctgtacg acgctacga gctgaagcac gccaaagctg gcgcggcac cgacgagaag 360
275 gtgctgaccg agatcatcgc ctcccgcacc ccgaggagc tgcgcgccat caagcaggcc 420
277 taccaggagg agtacggctc caacctggag gacgacgtgg tgggcgacac ctccggctac 480
279 taccagcgca tgctggtggt gctgtgacg gccaacccgc accccgacac cgccatcgac 540
281 gacgcccagg tggagctgga cgcccaggcc ctgttccagg ccggcgagct gaagtggggc 600
283 accgacgagg agaagttcat caccatcctg ggcacccgct ccgtgtccca cctgcgcgcg 660
285 gtgttcgaca agtacatgac catctccggc ttccagatcg aggagaccat cgaccgagag 720
287 acctccggca acctggagaa cctgtgtctg gccgtggtga agtccatccg ctccatcccc 780
289 gcctacctgg ccgagaccct gtactacgcc atgaagggcg ccggcaccga cgaccacacc 840
291 ctgatcccg tgatcgtgtc ccgctccgag atcgacctgt tcaacatccg caaggagttc 900
293 cgcaagaact tcgccacctc cctgtactcc atgatcaagg gcgacacctc cggcgactac 960
--> 295 aagaaggccc tgctgtgtgt gtgcggcgcc gaggacgacn nnagatctcg atcgggcctg 1020
--> 297 gaggtgctgt tccagggccc cggaagtact nnngccctgc gcggcaccgt gaccgacttc 1080
299 tccggcttcg acggccgcgc cgacgccgag gtgctgcgca aggccatgaa gggcctgggc 1140
301 accgacgagg actccatcct gaacctgctg accgcccgt ccaacgccc a ggcagcag 1200
303 atcgccgagg agttcaagac cctgttcggc cgcgacctgg tgaacgacat gaagtccgag 1260
305 ctgaccggca agttcgagaa gctgatcgtg gccctgatga agccctccc cctgtacgac 1320
307 gcctacgagc tgaagcacgc caagctgggc gccggcaccg acgagaaggt gctgaccgag 1380
309 atcatcgct cccgcacccc cgaggagctg cgcgccatca agcaggccta cgaggaggag 1440
311 tacggctcca acctggagga cgacgtggtg ggcgacacct ccggctacta ccagcgcag 1500

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313 ctggtggtgc tgctgcaggc caaccgcgac cccgacaccg ccatcgacga cgcccaggtg 1560
315 gagctggacg cccagggcct gttccaggcc ggcgagctga agtggggcac cgacgaggag 1620
317 aagttcatca ccatectggg caccgcgtcc gtgtcccacc tgcgcgcgt gttcgacaag 1680
319 tacatgacca tctccggctt ccagatcgag gagaccatcg accgcgagac ctccggcaac 1740
321 ctggagaacc tgctgctggc cgtggtgaag tccatccgct ccatccccgc ctacctggcc 1800
323 gagaccctgt actacgccat gaaggcgcc ggcaccgacg accacaccct gatccgcgtg 1860
325 atcgtgtccc gctccgagat cgacctgttc aacatccgca aggagttccg caagaacttc 1920
327 gccacctccc tgtactccat gatcaagggc gacacctccg gcgactacaa gaaggccctg 1980
329 ctgctgctgt gcggcggcga ggacgactaa taataa 2016
332 <210> SEQ ID NO: 5
333 <211> LENGTH: 2016
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial Sequence
337 <220> FEATURE:
338 <223> OTHER INFORMATION: primer
341 <220> FEATURE:
342 <221> NAME/KEY: CDS
343 <222> LOCATION: (1)..(2016)
345 <220> FEATURE:
346 <221> NAME/KEY: misc_feature
347 <222> LOCATION: (45)..(45)
348 <223> OTHER INFORMATION: n = a, c, t, or g
350 <220> FEATURE:
351 <221> NAME/KEY: misc_feature
352 <222> LOCATION: (1000)..(1002)
353 <223> OTHER INFORMATION: n = a, c, t, or g
355 <220> FEATURE:
356 <221> NAME/KEY: misc_feature
357 <222> LOCATION: (1051)..(1053)
358 <223> OTHER INFORMATION: n = a, c, t, or g
360 <400> SEQUENCE: 5
-> 361 atg gac tac aaa gac gat gac gac aag ctt gcg gcc gcg aat tcn gcc 48
-> 362 Met Asp Tyr Lys Asp Asp Asp Asp Lys Leu Ala Ala Ala Asn Xaa Ala
363 1 5 10 15
365 ctg cgc ggc acc gtg acc gac ttc tcc ggc ttc gac ggc cgc gcc gac 96
366 Leu Arg Gly Thr Val Thr Asp Phe Ser Gly Phe Asp Gly Arg Ala Asp
367 20 25 30
369 gcc gag gtg ctg cgc aag gcc atg aag ggc ctg ggc acc gac gag gac 144
370 Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp
371 35 40 45
373 tcc atc ctg aac ctg ctg acc gcc cgc tcc aac gcc cag cgc cag cag 192
374 Ser Ile Leu Asn Leu Leu Thr Ala Arg Ser Asn Ala Gln Arg Gln Gln
375 50 55 60
377 atc gcc gag gag ttc aag acc ctg ttc ggc cgc gac ctg gtg aac gac 240
378 Ile Ala Glu Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asn Asp
379 65 70 75 80
381 atg aag tcc gag ctg acc ggc aag ttc gag aag ctg atc gtg gcc ctg 288
382 Met Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu
383 85 90 95

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Please Note:

Sequence of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

q#:4; N Pos. ~~45,1000,1001,1002,1051,1052,1053~~
q#:5; N Pos. ~~45,1000,1001,1002,1051,1052,1053~~
q#:5; Xaa Pos. 15,334,351
q#:6; Xaa Pos. 15,334,351

Invalid <213> Response:

Sequence of "Artificial" only as "<213> Organism" response is incomplete,
or 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

q#:9

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0

L:295 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:960

L:297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1020

L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0

L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:48

L:441 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:960

L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1008

L:445 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1008

L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:1056

L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0

L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:320

L:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:336